

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 10/520,258 A  
Source: EFW  
Date Processed by STIC: 4-3-06

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IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/520,258A

DATE: 04/03/2006  
TIME: 15:13:12

Input Set : A:\20050-00003.ST25.txt  
Output Set: N:\CRF4\04032006\J520258A.raw

3 <110> APPLICANT: NEXGEN BIOTECHNOLOGIES, INC.  
4 SHONG, Min-Ho  
5 LEE, Sun  
6 YOO, Jae-Geun  
7 JIN, Seok-Min  
9 <120> TITLE OF INVENTION: Production of Transformed Plants Expressing Thyroid Stimulating Hormone Receptor  
12 <130> FILE REFERENCE: 20050-00003  
14 <140> CURRENT APPLICATION NUMBER: US 10/520,258A  
C--> 15 <141> CURRENT FILING DATE: 2005-01-03  
17 <150> PRIOR APPLICATION NUMBER: KR 2002-38064  
18 <151> PRIOR FILING DATE: 2002-07-02  
20 <150> PRIOR APPLICATION NUMBER: PCT/KR2003/001308  
21 <151> PRIOR FILING DATE: 2003-07-02  
23 <160> NUMBER OF SEQ ID NOS: 5  
25 <170> SOFTWARE: PatentIn version 3.3  
27 <210> SEQ ID NO: 1  
28 <211> LENGTH: 2292  
29 <212> TYPE: DNA  
30 <213> ORGANISM: Homo sapiens  
33 <220> FEATURE:  
34 <221> NAME/KEY: CDS  
35 <222> LOCATION: (1)..(2289)  
37 <400> SEQUENCE: 1  
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39 Met Arg Pro Ala Asp Leu Leu Gln Leu Val Leu Leu Leu Asp Leu Pro  
40 1 5 10 15  
42 agg gac ctg ggc gga atg ggg tgt tcg tct cca ccc tgc gag tgc cat 96  
43 Arg Asp Leu Gly Gly Met Gly Cys Ser Ser Pro Pro Cys Glu Cys His  
44 20 25 30  
46 cag gag gag gac ttc aga gtc acc tgc aag gat att caa cgc atc ccc 144  
47 Gln Glu Asp Phe Arg Val Thr Cys Lys Asp Ile Gln Arg Ile Pro  
48 35 40 45  
50 agc tta ccg ccc agt acg cag act ctg aag ctt att gag act cac ctg 192  
51 Ser Leu Pro Pro Ser Thr Gln Thr Leu Lys Leu Ile Glu Thr His Leu  
52 50 55 60  
54 aga act att cca agt cat gca ttt tct aat ctg ccc aat att tcc aga 240  
55 Arg Thr Ile Pro Ser His Ala Phe Ser Asn Leu Pro Asn Ile Ser Arg  
56 65 70 75 80  
58 atc tac gta tct ata gat gtg act ctg cag cag ctg gaa tca cac tcc 288  
59 Ile Tyr Val Ser Ile Asp Val Thr Leu Gln Gln Leu Glu Ser His Ser  
60 85 90 95  
62 ttc tac aat ttg agt aaa gtg act cac ata gaa att cgg aat acc agg 336

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63	Phe	Tyr	Asn	Leu	Ser	Lys	Val	Thr	His	Ile	Glu	Ile	Arg	Asn	Thr	Arg	
64				100				105							110		
66	aac	tta	act	tac	ata	gac	cct	gat	gcc	ctc	aaa	gag	ctc	ccc	ctc	cta	384
67	Asn	Leu	Thr	Tyr	Ile	Asp	Pro	Asp	Ala	Leu	Lys	Glu	Leu	Pro	Leu	Leu	
68				115				120							125		
70	aag	tcc	ttg	gca	ttt	tca	aac	act	gga	ctt	aaa	atg	ttc	cct	gac	ctg	432
71	Lys	Ser	Leu	Ala	Phe	Ser	Asn	Thr	Gly	Leu	Lys	Met	Phe	Pro	Asp	Leu	
72				130				135							140		
74	acc	aaa	gtt	tat	tcc	act	gat	ata	ttc	ttt	ata	ctt	gaa	att	aca	gac	480
75	Thr	Lys	Val	Tyr	Ser	Thr	Asp	Ile	Phe	Phe	Ile	Leu	Glu	Ile	Thr	Asp	
76	145				150						155				160		
78	aac	cct	tac	atg	acg	tca	atc	cct	gtg	aat	gct	ttt	cag	gga	cta	tgc	528
79	Asn	Pro	Tyr	Met	Thr	Ser	Ile	Pro	Val	Asn	Ala	Phe	Gln	Gly	Leu	Cys	
80					165				170						175		
82	aat	gaa	acc	ttg	aca	ctg	aag	ctg	tac	aac	aat	ggc	ttt	act	tca	gtc	576
83	Asn	Glu	Thr	Leu	Thr	Leu	Lys	Leu	Tyr	Asn	Asn	Gly	Phe	Thr	Ser	Val	
84				180				185							190		
86	caa	gga	tat	gtt	ttc	ttt	ggg	aca	aag	ctg	gat	gct	gtt	tac	cta	aac	624
87	Gln	Gly	Tyr	Asp	Phe	Phe	Gly	Thr	Lys	Leu	Asp	Ala	Val	Tyr	Leu	Asn	
88				195			200				205						
90	aag	aat	aaa	tac	ctg	aca	gtt	att	gac	aaa	gat	gca	ttt	gga	gga	gtt	672
91	Lys	Asn	Lys	Tyr	Leu	Thr	Val	Ile	Asp	Lys	Asp	Ala	Phe	Gly	Gly	Val	
92				210			215				220						
94	tac	agt	gga	cca	agc	ttg	ctg	gac	gtg	tct	caa	acc	agt	gtc	act	gcc	720
95	Tyr	Ser	Gly	Pro	Ser	Leu	Leu	Asp	Val	Ser	Gln	Thr	Ser	Val	Thr	Ala	
96	225				230					235					240		
98	ctt	cca	tcc	aaa	ggc	ctg	gag	cac	ctg	aag	gaa	ctg	ata	gca	aga	aac	768
99	Leu	Pro	Ser	Lys	Gly	Leu	Glu	His	Leu	Lys	Glu	Leu	Ile	Ala	Arg	Asn	
100					245			250				255					
102	agc	tgg	act	ctt	aag	aaa	ctt	gca	ctt	tcc	ttg	agt	ttc	ctt	cac	ctc	816
103	Ser	Trp	Thr	Leu	Lys	Lys	Leu	Ala	Leu	Ser	Leu	Ser	Phe	Leu	His	Leu	
104				260				265				270					
106	aca	cg	gct	gac	ctt	tct	tac	cca	agc	cac	tgc	tgt	gct	ttt	aag	aat	864
107	Thr	Arg	Ala	Asp	Leu	Ser	Tyr	Pro	Ser	His	Cys	Cys	Ala	Phe	Lys	Asn	
108				275			280				285						
110	cag	aag	aaa	atc	aga	gga	atc	ctt	gag	tcc	ttg	atg	tgt	aat	gag	agc	912
111	Gln	Lys	Lys	Ile	Arg	Gly	Ile	Leu	Glu	Ser	Leu	Met	Cys	Asn	Glu	Ser	
112				290			295				300						
114	agt	atc	gag	acg	ttg	cgc	cag	aga	aaa	tct	gtg	aat	gcc	ttg	aat	agc	960
115	Ser	Ile	Glu	Thr	Leu	Arg	Gln	Arg	Lys	Ser	Val	Asn	Ala	Leu	Asn	Ser	
116	305				310					315					320		
118	ccc	ctc	cac	cag	gaa	tat	gaa	gag	aat	ctg	ggt	gac	agc	att	gtt	ggg	1008
119	Pro	Leu	His	Gln	Glu	Tyr	Glu	Glu	Asn	Leu	Gly	Asp	Ser	Ile	Val	Gly	
120					325			330				335					
122	tac	aag	gaa	aag	tcc	aag	tcc	cag	gat	act	cat	aac	aac	gct	cat	tat	1056
123	Tyr	Lys	Glu	Lys	Ser	Lys	Phe	Gln	Asp	Thr	His	Asn	Asn	Ala	His	Tyr	
124				340				345				350					
126	tac	gtc	ttc	ttt	gaa	gaa	caa	gag	gat	gag	atc	att	ggt	ttt	ggc	cag	1104
127	Tyr	Val	Phe	Phe	Glu	Glu	Gln	Glu	Asp	Glu	Ile	Ile	Gly	Phe	Gly	Gln	

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128	355	360	365	
130	gag ctc aaa aac ccc cag	gaa gag act cta caa gct	ttt gac agc cat	1152
131	Glu Leu Lys Asn Pro Gln	Glu Glu Thr Leu Gln Ala	Phe Asp Ser His	
132	370	375	380	
134	tat gac tac acc ata tgt	ggg gac agt gaa gac	atg gtg tgt acc ccc	1200
135	Tyr Asp Tyr Thr Ile Cys	Gly Asp Ser Glu Asp	Met Val Cys Thr Pro	
136	385	390	395	400
138	aag tcc gat gag ttc aac	ccg tgt gaa gac ata	atg ggc tac aag ttc	1248
139	Lys Ser Asp Glu Phe Asn	Pro Cys Glu Asp Ile	Met Gly Tyr Lys Phe	
140	405	410	415	
142	ctg aga att gtg gtg tgg	ttc gtt agt ctg ctg	gct ctc ctg ggc aat	1296
143	Leu Arg Ile Val Val Trp	Phe Val Ser Leu Leu Ala	Leu Gly Asn	
144	420	425	430	
146	gtc ttt gtc ctg ctt att	ctc ctc acc agc cac	tac aaa ctg aac gtc	1344
147	Val Phe Val Leu Ile Leu	Leu Thr Ser His Tyr	Lys Leu Asn Val	
148	435	440	445	
150	ccc cgc ttt ctc atg tgc	aac ctg gcc ttt gcg	gat ttc tgc atg ggg	1392
151	Pro Arg Phe Leu Met Cys	Asn Leu Ala Phe Ala	Asp Phe Cys Met Gly	
152	450	455	460	
154	atg tac ctg ctc atc	gcc tct gta gac ctc	tac act cac tct gag	1440
155	Met Tyr Leu Leu Ile Ala	Ser Val Asp Leu Tyr	Thr His Ser Glu	
156	465	470	475	480
158	tac tac aac cat gcc atc	gac tgg cag aca ggc	cct ggg tgc aac acg	1488
159	Tyr Tyr Asn His Ala Ile	Asp Trp Gln Thr Gly	Pro Gly Cys Asn Thr	
160	485	490	495	
162	gct ggt ttc ttc act gtc	ttt gca agc gag tta	tgc gtg tat acg ctg	1536
163	Ala Gly Phe Phe Thr Val	Phe Ala Ser Glu Leu	Ser Val Tyr Thr Leu	
164	500	505	510	
166	acg gtc atc acc ctg gag	cgc tgg tat gcc atc	acc ttc gcc atg gcc	1584
167	Thr Val Ile Thr Leu Glu	Arg Trp Tyr Ala Ile	Thr Phe Ala Met Ala	
168	515	520	525	
170	ctg gac cgg aag atc cgc	ctc agg cac gca tgt	gcc atc atg gtt ggg	1632
171	Leu Asp Arg Lys Ile Arg	Leu Arg His Ala Cys	Ala Ile Met Val Gly	
172	530	535	540	
174	ggc tgg gtt tgc tgc ttc	ctt ctc gcc ctg ctt	cct ttg gtg gga ata	1680
175	Gly Trp Val Cys Cys Phe	Leu Leu Ala Leu Leu	Pro Leu Val Gly Ile	
176	545	550	555	560
178	agt agc tat gcc aaa gtc	agt atc tgc ctg ccc	atg gac acc gag acc	1728
179	Ser Ser Tyr Ala Lys Val	Ser Ile Cys Leu Pro	Met Asp Thr Glu Thr	
180	565	570	575	
182	cct ctt gct ctg gca tat	att gtt ttt gtt ctg	acg ctc aac ata gtt	1776
183	Pro Leu Ala Leu Ala	Tyr Ile Val Phe Val	Leu Thr Leu Asn Ile Val	
184	580	585	590	
186	gcc ttc gtc atc gtc tgc	tgc tgc tgt tat gtg	aag atc tac atc aca gtc	1824
187	Ala Phe Val Ile Val Cys	Cys Cys Tyr Val Lys	Ile Tyr Ile Thr Val	
188	595	600	605	
190	cga aat ccg cac aac cca	ggg gac aaa gat acc	aaa att gcc aag agg	1872
191	Arg Asn Pro His Asn Pro	Gly Asp Lys Asp Thr	Lys Ile Ala Lys Arg	
192	610	615	620	

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194 atg gct gtg ttg atc ttc acc gac ttc acg tgc atg gcc cca atc tca	1920
195 Met Ala Val Leu Ile Phe Thr Asp Phe Thr Cys Met Ala Pro Ile Ser	
196 625 630 635 640	
198 ttc tat gct gtg tca gca att ctg aac aag cct ctc atc act gtt agc	1968
199 Phe Tyr Ala Val Ser Ala Ile Leu Asn Lys Pro Leu Ile Thr Val Ser	
200 645 650 655	
202 aac tcc aaa atc ttg ctg gta ctc ttc tat cca att aac tcc tgt gcc	2016
203 Asn Ser Lys Ile Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser Cys Ala	
204 660 665 670	
206 aat cca ttc ctc tat gct att ttc acc aag gcc ttc cag agg gat gtg	2064
207 Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Ala Phe Gln Arg Asp Val	
208 675 680 685	
210 ttc atc cta ctc agc aag ttt ggc atc tgt aaa cgc cag gct cag gca	2112
211 Phe Ile Leu Leu Ser Lys Phe Gly Ile Cys Lys Arg Gln Ala Gln Ala	
212 690 695 700	
214 tac cgg ggg cag agg gtt cct cca aag aac agc act gat att cag gtt	2160
215 Tyr Arg Gly Gln Arg Val Pro Pro Lys Asn Ser Thr Asp Ile Gln Val	
216 705 710 715 720	
218 caa aag gtt acc cac gac atg agg cag ggt ctc cac aac atg gaa gat	2208
219 Gln Lys Val Thr His Asp Met Arg Gln Gly Leu His Asn Met Glu Asp	
220 725 730 735	
222 gtc tat gaa ctg att gaa aac tcc cat cta acc cca aag aag caa ggc	2256
223 Val Tyr Glu Leu Ile Glu Asn Ser His Leu Thr Pro Lys Lys Gln Gly	
224 740 745 750	
226 caa atc tca gaa gag tat atg caa acg gtt ttg taa	2292
227 Gln Ile Ser Glu Glu Tyr Met Gln Thr Val Leu	
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233 <212> TYPE: PRT	
234 <213> ORGANISM: Homo sapiens	
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243 20 25 30	
246 Gln Glu Glu Asp Phe Arg Val Thr Cys Lys Asp Ile Gln Arg Ile Pro	
247 35 40 45	
250 Ser Leu Pro Pro Ser Thr Gln Thr Leu Lys Leu Ile Glu Thr His Leu	
251 50 55 60	
254 Arg Thr Ile Pro Ser His Ala Phe Ser Asn Leu Pro Asn Ile Ser Arg	
255 65 70 75 80	
258 Ile Tyr Val Ser Ile Asp Val Thr Leu Gln Gln Leu Glu Ser His Ser	
259 85 90 95	
262 Phe Tyr Asn Leu Ser Lys Val Thr His Ile Glu Ile Arg Asn Thr Arg	
263 100 105 110	
266 Asn Leu Thr Tyr Ile Asp Pro Asp Ala Leu Lys Glu Leu Pro Leu Leu	
267 115 120 125	
270 Lys Ser Leu Ala Phe Ser Asn Thr Gly Leu Lys Met Phe Pro Asp Leu	

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271	130	135	140
274	Thr Lys Val Tyr Ser Thr Asp Ile Phe Phe Ile Leu Glu Ile Thr Asp		
275	145	150	155
278	Asn Pro Tyr Met Thr Ser Ile Pro Val Asn Ala Phe Gln Gly Leu Cys		160
279	165	170	175
282	Asn Glu Thr Leu Thr Leu Lys Leu Tyr Asn Asn Gly Phe Thr Ser Val		
283	180	185	190
286	Gln Gly Tyr Asp Phe Phe Gly Thr Lys Leu Asp Ala Val Tyr Leu Asn		
287	195	200	205
290	Lys Asn Lys Tyr Leu Thr Val Ile Asp Lys Asp Ala Phe Gly Gly Val		
291	210	215	220
294	Tyr Ser Gly Pro Ser Leu Leu Asp Val Ser Gln Thr Ser Val Thr Ala		
295	225	230	235
298	Leu Pro Ser Lys Gly Leu Glu His Leu Lys Glu Leu Ile Ala Arg Asn		240
299	245	250	255
302	Ser Trp Thr Leu Lys Lys Leu Ala Leu Ser Leu Ser Phe Leu His Leu		
303	260	265	270
306	Thr Arg Ala Asp Leu Ser Tyr Pro Ser His Cys Cys Ala Phe Lys Asn		
307	275	280	285
310	Gln Lys Lys Ile Arg Gly Ile Leu Glu Ser Leu Met Cys Asn Glu Ser		
311	290	295	300
314	Ser Ile Glu Thr Leu Arg Gln Arg Lys Ser Val Asn Ala Leu Asn Ser		
315	305	310	315
318	320		
319	Pro Leu His Gln Glu Tyr Glu Glu Asn Leu Gly Asp Ser Ile Val Gly		
322	325	330	335
323	Tyr Lys Glu Lys Ser Lys Phe Gln Asp Thr His Asn Asn Ala His Tyr		
326	340	345	350
327	Tyr Val Phe Phe Glu Glu Gln Glu Asp Glu Ile Ile Gly Phe Gly Gln		
330	355	360	365
331	Glu Leu Lys Asn Pro Gln Glu Glu Thr Leu Gln Ala Phe Asp Ser His		
334	370	375	380
335	Tyr Asp Tyr Thr Ile Cys Gly Asp Ser Glu Asp Met Val Cys Thr Pro		
338	385	390	395
339	Lys Ser Asp Glu Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Lys Phe		400
342	405	410	415
343	Leu Arg Ile Val Val Trp Phe Val Ser Leu Leu Ala Leu Leu Gly Asn		
346	420	425	430
347	Val Phe Val Leu Leu Ile Leu Thr Ser His Tyr Lys Leu Asn Val		
350	435	440	445
351	Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp Phe Cys Met Gly		
354	450	455	460
355	Met Tyr Leu Leu Leu Ile Ala Ser Val Asp Leu Tyr Thr His Ser Glu		
358	465	470	475
359	Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Pro Gly Cys Asn Thr		480
362	485	490	495
363	Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu		
366	500	505	510
367	Thr Val Ile Thr Leu Glu Arg Trp Tyr Ala Ile Thr Phe Ala Met Ala		
	515	520	525

**VERIFICATION SUMMARY**

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date